1 : 1

14

2 . 2

## SEQUENCE LISTING

```
SEQ ID NO: 1 is primate GPR2 nucleotide sequence.
     SEQ ID NO: 2 is primate GPR2 amino acid sequence.
     SEQ ID NO: 3 is rodent GPR2 nucleotide sequence.
     SEQ ID NO: 4 is rodent GPR2 amino acid sequence.
     SEQ ID NO: 5 is primate Vic nucleotide sequence.
10
     SEQ ID NO: 6 is primate Vic amino acid sequence.
     SEQ ID NO: 7 is alternative primate Vic nucleotide sequence.
     SEQ ID NO: 8 is alternative primate Vic amino acid sequence.
     SEQ ID NO: 9 is rodent Vic nucleotide sequence.
     SEQ ID NO: 10 is rodent Vic amino acid sequence.
     SEQ ID NO: 11 is primate CTACK nucleotide sequence.
15
     SEQ ID NO: 12 is primate CTACK amino acid sequence.
     SEQ ID NO: 13 is rodent CTACK nucleotide sequence.
     SEQ ID NO: 14 is rodent CTACK amino acid sequence.
     SEQ ID NO: 15 provides a primate actin PCR primer sequence.
     SEQ ID NO: 16 provides a primate actin PCR primer sequence.
20
     <110> Wang, Wei
           Oldham, Elizabeth R.
           Soto, Hortensia
25
           Liu, Ying
           Hudak, Susan A.
           Homey, Bernhard
           Morales, Janine M.
           Kellermann, Sirid-Aimee
30
           McEvoy, Leslie M.
           Bowman, Edward P.
           Zlotnik, Albert
     <120> Chemokine and Receptor Uses; Compositions; Methods
35
     <130> DX0882XK
     <140>
     <141>
40
     <160> 16
     <170> PatentIn Ver. 2.0
45
     <210> 1
     <211> 1089
     <212> DNA
     <213> primate
50
     <220>
     <221> CDS
     <222> (1)..(1086)
     <400> 1
55
```

5						tta Leu											48
J	gat Asp	gaa Glu	gag Glu	gac Asp 20	gca Ala	tac Tyr	tcg Ser	gct Ala	gag Glu 25	cca Pro	ctg Leu	ccg Pro	gag Glu	ctt Leu 30	tgc Cys	tac Tyr	96
10						gcc Ala											144
15	ctg Leu	acg Thr 50	ctg Leu	gct Ala	gcg Ala	ctg Leu	ggt Gly 55	ctg Leu	gcc Ala	ggc Gly	aat Asn	ggc Gly 60	ctg Leu	gtc Val	ctg Leu	gcc Ala	192
20	acc Thr 65	cac His	ctg Leu	gca Ala	gcc Ala	cga Arg 70	cgc Arg	gca Ala	gcg Ala	cgc Arg	tcg Ser 75	ccc Pro	acc Thr	tct Ser	gcc Ala	cac His 80	240
25	ctg Leu	ctc Leu	cag Gln	ctg Leu	gcc Ala 85	ctg Leu	gcc Ala	gac Asp	ctc Leu	ttg Leu 90	ctg Leu	gcc Ala	ctg Leu	act Thr	ctg Leu 95	ccc Pro	288
23	ttc Phe	gcg Ala	gca Ala	gca Ala 100	Gly 999	gct Ala	ctt Leu	cag Gln	ggc Gly 105	tgg Trp	agt Ser	ctg Leu	gga Gly	agt Ser 110	gcc Ala	acc Thr	336
30	tgc Cys	cgc Arg	acc Thr 115	atc Ile	tct Ser	ggc Gly	ctc Leu	tac Tyr 120	tcg Ser	gcc Ala	tcc Ser	ttc Phe	cac His 125	gcc Ala	ggc Gly	ttc Phe	384
35	ctc Leu	ttc Phe 130	ctg Leu	gcc Ala	tgt Cys	atc Ile	agc Ser 135	gcc Ala	gac Asp	cgc Arg	tac Tyr	gtg Val 140	gcc Ala	atc Ile	gcg Ala	cga Arg	432
40	gcg Ala 145	ctc Leu	cca Pro	gcc Ala	gly ggg	ccg Pro 150	cgg Arg	ccc Pro	tcc Ser	act Thr	ccc Pro 155	ggc Gly	cgc Arg	gca Ala	cac His	ttg Leu 160	480
45	gtc Val	tcc Ser	gtc Val	atc Ile	gtg Val 165	tgg Trp	ctg Leu	ctg Leu	tca Ser	ctg Leu 170	ctc Leu	ctg Leu	gcg Ala	ctg Leu	cct Pro 175	gcg Ala	528
43	ctg Leu	ctc Leu	ttc Phe	agc Ser 180	cag Gln	gat Asp	ggg Gly	cag Gln	cgg Arg 185	gaa Glu	ggc Gly	caa Gln	cga Arg	cgc Arg 190	tgt Cys	cgc Arg	576
50	ctc Leu	atc Ile	ttc Phe 195	ccc Pro	gag Glu	ggc Gly	ctc Leu	acg Thr 200	cag Gln	acg Thr	gtg Val	aag Lys	999 Gly 205	gcg Ala	agc Ser	gcc Ala	624
55	gtg Val	gcg Ala 210	cag Gln	gtg Val	gcc Ala	ctg Leu	ggc Gly 215	ttc Phe	gcg Ala	ctg Leu	ccg Pro	ctg Leu 220	ggc Gly	gtc Val	atg Met	gta Val	672

The first first state and the first state of the state of the first st

and the contraction of part of the contraction of t

5	gcc Ala 225	tgc Cys	tac Tyr	gcg Ala	ctt Leu	ctg Leu 230	ggc Gly	cgc Arg	acg Thr	ctg Leu	ctg Leu 235	gcc Ala	gcc Ala	agg Arg	Gly 999	ccc Pro 240	720
5	gag Glu	cgc Arg	cgg Arg	cgt Arg	gcg Ala 245	ctg Leu	cgc Arg	gtc Val	gtg Val	gtg Val 250	gct Ala	ctg Leu	gtg Val	gcg Ala	gcc Ala 255	ttc Phe	768
10	gtg Val	gtg Val	ctg Leu	cag Gln 260	ctg Leu	ccc Pro	tac Tyr	agc Ser	ctc Leu 265	gcc Ala	ctg Leu	ctg Leu	ctg Leu	gat Asp 270	act Thr	gcc Ala	816
15	gat Asp	cta Leu	ctg Leu 275	gct Ala	gcg Ala	cgc Arg	gag Glu	cgg Arg 280	agc Ser	tgc Cys	cct Pro	gcc Ala	agc Ser 285	aaa Lys	cgc Arg	aag Lys	864
20	gat Asp	gtc Val 290	gca Ala	ctg Leu	ctg Leu	gtg Val	acc Thr 295	agc Ser	ggc Gly	ttg Leu	gcc Ala	ctc Leu 300	gcc Ala	cgc Arg	tgt Cys	ggc Gly	912
	ctc Leu 305	aat Asn	ccc Pro	gtt Val	ctc Leu	tac Tyr 310	gcc Ala	ttc Phe	ctg Leu	ggc Gly	ctg Leu 315	cgc Arg	ttc Phe	cgc Arg	cag Gln	gac Asp 320	960
25	ctg Leu	cgg Arg	agg Arg	ctg Leu	cta Leu 325	cgg Arg	ggt Gly	ggg Gly	agc Ser	tcg Ser 330	ccc Pro	tca Ser	Gly ggg	cct Pro	caa Gln 335	ccc Pro	1008
30	cgc Arg	cgc Arg	ggc Gly	tgc Cys 340	ccc Pro	cgc Arg	cgg Arg	ccc Pro	cgc Arg 345	ctt Leu	tct Ser	tcc Ser	tgc Cys	tca Ser 350	gct Ala	ccc Pro	1056
35		gag Glu									tag						1089
40	<21 <21	0 > 2 1 > 3 + 2 > P: 3 > p:	RT	te													
45		0> 2 Gly	Thr	Glu	Val 5	Leu	Glu	Gln	Val	Ser 10	Trp	Gly	His	Tyr	Ser 15	Gly	
	Asp	Glu	Glu	Asp 20	Ala	Tyr	Ser	Ala	Glu 25	Pro	Leu	Pro	Glu	Leu 30	Cys	Tyr	
50	Lys	Ala	Asp 35	Val	Gln	Ala	Phe	Ser 40		Ala	Phe	Gln	Pro 45	Ser	Val	Ser	
55	Leu	Thr 50	Leu	Ala	Ala	Leu	Gly 55	Leu	Ala	Gly	Asn	Gly 60	Leu	Val	Leu	Ala	
	Thr 65	His	Leu	Ala	Ala	Arg 70	Arg	Ala	Ala	Arg	Ser 75	Pro	Thr	Ser	Ala	His 80	

	Leu	Leu	Gln	Leu	Ala 85	Leu	Ala	Asp	Leu	Leu 90	Leu	Ala	Leu	Thr	Leu 95	Pro
5	Phe	Ala	Ala	Ala 100	Gly	Ala	Leu	Gln	Gly 105	Trp	Ser	Leu	Gly	Ser 110	Ala	Thr
10	Cys	Arg	Thr 115	Ile	Ser	Gly	Leu	Tyr 120	Ser	Ala	Ser	Phe	His 125	Ala	Gly	Phe
	Leu	Phe 130	Leu	Ala	Cys	Ile	Ser 135	Ala	Asp	Arg	Tyr	Val 140	Ala	Ile	Ala	Arg
15	Ala 145	Leu	Pro	Ala	Gly	Pro 150	Arg	Pro	Ser	Thr	Pro 155	Gly	Arg	Ala	His	Leu 160
	Val	Ser	Val	Ile	Val 165	Trp	Leu	Leu	Ser	Leu 170	Leu	Leu	Ala	Leu	Pro 175	Ala
20	Leu	Leu	Phe	Ser 180	Gln	Asp	Gly	Gln	Arg 185	Glu	Gly	Gln	Arg	Arg 190	Cys	Arg
25	Leu	Ile	Phe 195	Pro	Glu	Gly	Leu	Thr 200	Gln	Thr	Val	Lys	Gly 205	Ala	Ser	Ala
	Val	Ala 210	Gln	Val	Ala	Leu	Gly 215	Phe	Ala	Leu	Pro	Leu 220	Gly	Val	Met	Val
30	Ala 225	Cys	Tyr	Ala	Leu	Leu 230	Gly	Arg	Thr	Leu	Leu 235	Ala	Ala	Arg	Gly	Pro 240
	Glu	Arg	Arg	Arg	Ala 245	Leu	Arg	Val	Val	Val 250	Ala	Leu	Val	Ala	Ala 255	Phe
35	Val	Val	Leu	Gln 260	Leu	Pro	Tyr	Ser	Leu 265	Ala	Leu	Leu	Leu	Asp 270	Thr	Ala
40	Asp	Leu	Leu 275	Ala	Ala	Arg	Glu	Arg 280	Ser	Cys	Pro	Ala	Ser 285	Lys	Arg	Lys
	Asp	Val 290	Ala	Leu	Leu	Val	Thr 295	Ser	Gly	Leu	Ala	Leu 300	Ala	Arg	Сув	Gly
45	Leu 305	Asn	Pro	Val	Leu	Tyr 310	Ala	Phe	Leu	Gly	Leu 315	Arg	Phe	Arg	Gln	Asp 320
	Leu	Arg	Arg	Leu	Leu 325	Arg	Gly	Gly	Ser	Ser 330	Pro	Ser	Gly	Pro	Gln 335	Pro
50	Arg	Arg	Gly	Cys 340	Pro	Arg	Arg	Pro	Arg 345	Leu	Ser	Ser	Cys	Ser 350	Ala	Pro
55	Thr	Glu	Thr 355	His	Ser	Leu	Ser	Trp 360	Asp	Asn						

<210> 3 <211> 1089 <212> DNA 5 <213> rodent <220> <221> CDS <222> (1)..(1086) 10 <400> 3 atg ggg acc aag ccc aca gag cag gtc tcc tgg gga ctt tac tcc ggg 48 Met Gly Thr Lys Pro Thr Glu Gln Val Ser Trp Gly Leu Tyr Ser Gly 15 tac gat gag gag gcc tat tcg gtt ggg ccg ctg cca gag ctc tgt tac 96 Tyr Asp Glu Glu Ala Tyr Ser Val Gly Pro Leu Pro Glu Leu Cys Tyr aag got gat gto cag got tto agt ogg god tto caa cod agt gto too 144 20 Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser 40 35 ctg atg gtg gct gta ctg ggt ctg gct ggc aat ggc cta gtc ttg gcc 192 Leu Met Val Ala Val Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala 25 55 50 acc cat ctg gca gcc aga cga act acc cga tct ccc acc tcc gtt cac 240 Thr His Leu Ala Ala Arg Arg Thr Thr Arg Ser Pro Thr Ser Val His 30 65 ctg ctc cag ttg gcc ctg gct gac ctt tta ttg gcc ctg act ttg cct 288 Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro 95 35 ttt gct gca gca ggg gct ctt cag ggc tgg aat cta gga agt acc acc 336 Phe Ala Ala Gly Ala Leu Gln Gly Trp Asn Leu Gly Ser Thr Thr 105 100 40 tgc cgt gcc atc tca ggc ctc tac tcg gcc tct ttc cac gct ggc ttc 384 Cys Arg Ala Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe 120 115 ctc ttc cta gcc tgt atc agc gcc gac cgc tat gtg gcc atc gca cga 432 45 Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg 135 130 get etc eca gee ggg cag egg ecc tea aeg eet age ega geg eac ttg 480 Ala Leu Pro Ala Gly Gln Arg Pro Ser Thr Pro Ser Arg Ala His Leu 50 150 145 gtt tca gtc ttc gtg tgg ctg ttg gcg ctg ttt ctg gct cta cct gcg 528 Val Ser Val Phe Val Trp Leu Leu Ala Leu Phe Leu Ala Leu Pro Ala 55 170 165

576

ctc ctt ttc agc cgg gac ggg cca cgt gaa ggc caa cga cgc tgt cgg

														Arg 190			576
5	ctc Leu	att Ile	ttt Phe 195	ccc Pro	gaa Glu	agc Ser	ctc Leu	acg Thr 200	cag Gln	act Thr	gtg Val	aaa Lys	999 Gly 205	gca Ala	agc Ser	gca Ala	624
10	gtg Val	gcg Ala 210	cag Gln	gtg Val	gtc Val	ctc Leu	ggc Gly 215	ttc Phe	gcg Ala	ctc Leu	cct Pro	ctg Leu 220	ggc Gly	gtc Val	atg Met	gca Ala	672
15	gcc Ala 225	tgt Cys	tat Tyr	gcg Ala	ctc Leu	ctg Leu 230	ggc Gly	cgc Arg	acg Thr	ctt Leu	ctg Leu 235	gcc Ala	gcc Ala	agg Arg	ggg Gly	cca Pro 240	720
20	gag Glu	cgg Arg	cgg Arg	cgt Arg	gca Ala 245	ctg Leu	cgc Arg	gtc Val	gtg Val	gtg Val 250	gct Ala	ttg Leu	gtg Val	gtg Val	gcc Ala 255	ttc Phe	768
20	gtg Val	gtg Val	ctg Leu	cag Gln 260	ttg Leu	ccc Pro	tac Tyr	agc Ser	ctt Leu 265	gcc Ala	ctg Leu	ctg Leu	ctg Leu	gat Asp 270	aca Thr	gcc Ala	816
25	gat Asp	cta Leu	ctg Leu 275	gca Ala	gcc Ala	cgc Arg	gag Glu	cgg Arg 280	agc Ser	tgc Cys	tcc Ser	tcc Ser	agc Ser 285	aag Lys	cgc Arg	aag Lys	864
30	gat Asp	cta Leu 290	gct Ala	ttg Leu	ctg Leu	gtc Val	acc Thr 295	ggc Gly	ggc Gly	ttg Leu	acc Thr	ctg Leu 300	gtc Val	cgt Arg	tgc Cys	agc Ser	912
35	ctc Leu 305	aat Asn	ccg Pro	gtg Val	ctt Leu	tat Tyr 310	gcc Ala	ttt Phe	ttg Leu	ggc Gly	ctg Leu 315	cgt Arg	ttc Phe	cgc Arg	cgg Arg	gac Asp 320	960
40	ctg Leu	cgg Arg	agg Arg	ctg Leu	ctc Leu 325	cag Gln	ggc Gly	gga Gly	gga Gly	tgc Cys 330	agc Ser	ccg Pro	aag Lys	ccc Pro	aac Asn 335	cct Pro	1008
40	cgt Arg	ggc Gly	cgc Arg	tgc Cys 340	ccc Pro	cgt Arg	cga Arg	ctc Leu	cgc Arg 345	ctt Leu	tct Ser	tcc Ser	tgc Cys	tct Ser 350	gct Ala	cct Pro	1056
45					agt Ser						tag						1089
50	<21 <21	0 > 4 1 > 3 2 > P 3 > r	RT	t													
55		0> 4 Gly	Thr	Lys	Pro	Thr	Glu	Gln	Val	Ser	Trp	Gly	Leu	Tyr	Ser	Gly	

10

15

error and many many are sense and event grown to the control of the first firs

	Tyr	Asp	Glu	Glu 20	Ala	Tyr	Ser	Val	Gly 25	Pro	Leu	Pro	Glu	Leu 30	Cys	Tyr
5	Lys	Ala	Asp 35	Val	Gln	Ala	Phe	Ser 40	Arg	Ala	Phe	Gln	Pro 45	Ser	Val	Ser
	Leu	Met 50	Val	Ala	Val	Leu	Gly 55	Leu	Ala	Gly	Asn	Gly 60	Leu	Val	Leu	Ala
10	Thr 65	His	Leu	Ala	Ala	Arg 70	Arg	Thr	Thr	Arg	Ser 75	Pro	Thr	Ser	Val	His 80
15	Leu	Leu	Gln	Leu	Ala 85	Leu	Ala	Asp	Leu	Leu 90	Leu	Ala	Leu	Thr	Leu 95	Pro
13	Phe	Ala	Ala	Ala 100	Gly	Ala	Leu	Gln	Gly 105	Trp	Asn	Leu	Gly	Ser 110	Thr	Thr
20	Cys	Arg	Ala 115	Ile	Ser	Gly	Leu	Tyr 120	Ser	Ala	Ser	Phe	His 125	Ala	Gly	Phe
	Leu	Phe 130	Leu	Ala	Cys	Ile	Ser 135	Ala	Asp	Arg	Tyr	Val 140	Ala	Ile	Ala	Arg
25	Ala 145	Leu	Pro	Ala	Gly	Gln 150	Arg	Pro	Ser	Thr	Pro 155	Ser	Arg	Ala	His	Leu 160
30	Val	Ser	Val	Phe	Val 165	Trp	Leu	Leu	Ala	Leu 170	Phe	Leu	Ala	Leu	Pro 175	Ala
30	Leu	Leu	Phe	Ser 180	Arg	Asp	Gly	Pro	Arg 185	Glu	Gly	Gln	Arg	Arg 190	Cys	Arg
35	Leu	Ile	Phe 195	Pro	Glu	Ser	Leu	Thr 200	Gln	Thr	Val	Lys	Gly 205	Ala	Ser	Ala
	Val	Ala 210	Gln	Val	Val	Leu	Gly 215	Phe	Ala	Leu	Pro	Leu 220	Gly	Val	Met	Ala
40	Ala 225	Cys	Tyr	Ala	Leu	Leu 230	Gly	Arg	Thr	Leu	Leu 235	Ala	Ala	Arg	Gly	Pro 240
45	Glu	Arg	Arg	Arg	Ala 245	Leu	Arg	Val	Val	Val 250	Ala	Leu	Val	Val	Ala 255	Phe
13	Val	Val	Leu	Gln 260	Leu	Pro	Tyr	Ser	Leu 265	Ala	Leu	Leu	Leu	Asp 270	Thr	Ala
50	Asp	Leu	Leu 275	Ala	Ala	Arg	Glu	Arg 280	Ser	Сув	Ser	Ser	Ser 285	Lys	Arg	Lys
	Asp	Leu 290	Ala	Leu	Leu	Val	Thr 295	Gly	Gly	Leu	Thr	Leu 300	Val	Arg	Cys	Ser
55	Leu 305		Pro	Val	Leu	Tyr 310	Ala	Phe	Leu	Gly	Leu 315	Arg	Phe	Arg	Arg	Asp 320

the design of the first state of the state o

	Leu Arg Arg	Leu Leu 325	Gln Gly	Gly	Gly	Cys 330	Ser	Pro	Lys	Pro	Asn 335	Pro	
5	Arg Gly Arg	Cys Pro 340	Arg Arg	Leu	Arg 345	Leu	Ser	Ser	Cys	Ser 350	Ala	Pro	
	Thr Glu Thr 355	His Ser	Leu Ser	Trp 360	Asp	Asn							
10	<210> 5 <211> 731 <212> DNA <213> prima	te											
15	<220> <221> CDS <222> (56).	. (436)											
20	<220> <221> mat_p <222> (122)	_											
25	<220> <221> misc_ <222> (529) <223> V; ma		C, or G										
30	<400> 5 ggctgatcga	acageetea	ac ttgtg	ttgct	t gto	agto	gcca	gtag	ggca	agg (	cagga	atg Met	58
35	cag cag aga Gln Gln Arg -20	gga ctc Gly Leu	gcc ato Ala Ile -15	Val	gcc Ala	ttg Leu	gct Ala	gtc Val -10	tgt Cys	gcg Ala	gcc Ala	cta Leu	106
33	cat gcc tca His Ala Ser -5	gaa gcc Glu Ala -1	ata ctt Ile Leu 1	ccc Pro	att Ile	gcc Ala 5	tcc Ser	agc Ser	tgt Cys	tgc Cys	acg Thr 10	gag Glu	154
40	gtt tca cat Val Ser His	cat att His Ile 15	tcc aga Ser Arg	agg Arg	ctc Leu 20	ctg Leu	gaa Glu	aga Arg	gtg Val	aat Asn 25	atg Met	tgt Cys	202
45	cgc atc cag Arg Ile Gln 30	Arg Ala	gat ggg Asp Gly	gat Asp 35	tgt Cys	gac Asp	ttg Leu	gct Ala	gct Ala 40	gtc Val	atc Ile	ctt Leu	250
50	cat gtc aag His Val Lys 45	cgc aga Arg Arg	aga ato Arg Ile 50	Cys	gtc Val	agc Ser	ccg Pro	cac His 55	aac Asn	cat His	act Thr	gtt Val	298
55	aag cag tgg Lys Gln Trp 60	atg aaa Met Lys	gtg caa Val Glr 65	gct Ala	gcc Ala	aag Lys	aaa Lys 70	aat Asn	ggt Gly	aaa Lys	gga Gly	aat Asn 75	346
55	gtt tgc cac Val Cys His	agg aag Arg Lys 80	aaa cac Lys His	cat His	ggc Gly	aag Lys 85	agg Arg	aac Asn	agt Ser	aac Asn	agg Arg 90	gca Ala	394

the first fi

55 <222> (1)..(492)

<400> 7

	cat cag ggg aaa cac gaa aca tac ggc cat aaa act cct tat His Gln Gly Lys His Glu Thr Tyr Gly His Lys Thr Pro Tyr 95 100 105	36
5	tagagagtet acagataaat etacagagae aatteeteaa gtggaettgg eeatgattgg 4	96
	ttgtcctgca tactgatgaa actactgatg tcvgctggtc tgaaaggacc taccagaagc 5	56
10	taaatotoca agaatgooat ttoootatoo otaatgatto aatotooott accotgacca 6	16
	atcagtggcc caaattttcc agccccttgc ctcccagaac cccagcccag	76
15	agatttaaga atctcctcct acctcctgac tcagccccat gtaatcatta aactc 7	731
20	<210> 6 <211> 127 <212> PRT <213> primate	
0.5	<pre>&lt;400&gt; 6 Met Gln Gln Arg Gly Leu Ala Ile Val Ala Leu Ala Val Cys Ala Ala</pre>	
25	Leu His Ala Ser Glu Ala Ile Leu Pro Ile Ala Ser Ser Cys Cys Thr -5 -1 1 5 10	
30	Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn Met 15 20 25	
	Cys Arg Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile 30 35 40	
35	Leu His Val Lys Arg Arg Ile Cys Val Ser Pro His Asn His Thr 45 50 55	
4.0	Val Lys Gln Trp Met Lys Val Gln Ala Ala Lys Lys Asn Gly Lys Gly 60 65 70	
40	Asn Val Cys His Arg Lys Lys His His Gly Lys Arg Asn Ser Asn Arg 75 80 85 90	
45	Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys Thr Pro Tyr 95 100 105	
50	<210> 7 <211> 543 <212> DNA <213> primate	
	<220> <221> CDS	

															gag Glu 15		48
5															tgg Trp		96
10															ctg Leu		144
15															act Thr		192
20															tgt Cys		240
20															att Ile 95		288
25	cac His	atg Met	gaa Glu	ctg Leu 100	cag Gln	gag Glu	gcc Ala	gat Asp	ggg Gly 105	gac Asp	tgt Cys	cac His	ctc Leu	cag Gln 110	gct Ala	gtc Val	336
30	gtg Val	ctt Leu	cac His 115	ctg Leu	gct Ala	cgg Arg	cgc Arg	agt Ser 120	gtc Val	tgt Cys	gtt Val	cat His	ccc Pro 125	cag Gln	aac Asn	cgc Arg	384
35	agc Ser	ctg Leu 130	gct Ala	cgg Arg	tgg Trp	tta Leu	gaa Glu 135	cgc Arg	caa Gln	Gly 999	aaa Lys	agg Arg 140	ctc Leu	caa Gln	Gly 999	act Thr	432
40															aac Asn		480
10		_	caa Gln		taat	aaag	gca a	acatt	agad	eg ad	caaaa	aaaa	a aaa	aaaa	aaaa		532
45	aaaa	aaaa	aaa a	a													543
50	<212	l> 16 2> PF		:e													
FF	<400 Met 1		Arg	Leu	Arg 5	Arg	Tyr	Glu	Val	Ala 10	Leu	Glu	Ala	Glu	Glu 15	Glu	
<b>5</b> 5	Ile	Tyr	Trp	Gly 20	Cys	Phe	Tyr	Phe	Phe 25	Pro	Trp	Leu	Arg	Met 30	Trp	Arg	

the first feet and the first feet of the f

Arg Glu Arg Ser Pro Met Ser Pro Thr Ser Gln Arg Leu Ser Leu Glu 40 35 Ala Pro Ser Leu Pro Leu Arg Ser Trp His Pro Trp Asn Lys Thr Lys 5 Gln Lys Gln Glu Ala Leu Pro Leu Pro Ser Ser Thr Ser Cys Cys Thr 70 10 Gln Leu Tyr Arg Gln Pro Leu Pro Ser Arg Leu Leu Arg Arg Ile Val 90 His Met Glu Leu Gln Glu Ala Asp Gly Asp Cys His Leu Gln Ala Val 15 Val Leu His Leu Ala Arg Arg Ser Val Cys Val His Pro Gln Asn Arg 120 Ser Leu Ala Arg Trp Leu Glu Arg Gln Gly Lys Arg Leu Gln Gly Thr 20 135 Val Pro Ser Leu Asn Leu Val Leu Gln Lys Lys Met Tyr Ser Asn Pro 155 25 Gln Gln Gln Asn 30 <210> 9 <211> 393 <212> DNA <213> rodent 35 <220> <221> CDS <222> (1)..(390) <220> 40 <221> mat peptide <222> (67)..(390) atg cag caa gca ggg ctc aca ctc atg gct gtg gct gtg tgt gtg gct Met Gln Gln Ala Gly Leu Thr Leu Met Ala Val Ala Val Cys Val Ala 45 -15 ttt caa acc tca gaa gcc ata ctt ccc atg gcc tcc agc tgt tgc act Phe Gln Thr Ser Glu Ala Ile Leu Pro Met Ala Ser Ser Cys Cys Thr 50 -1 gag gtg tct cat cat gtt tcc gga aga ctt ctg gaa aga gtg agt tca Glu Val Ser His His Val Ser Gly Arg Leu Leu Glu Arg Val Ser Ser 15 55

tgc agc atc cag aga gct gac ggg gac tgc gac ctg gct gct gtc atc Cys Ser Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile

5	ctt Leu	cat His	gtt Val 45	aaa Lys	cgt Arg	aga Arg	aga Arg	atc Ile 50	tgc Cys	atc Ile	agc Ser	ccg Pro	cac His 55	aat Asn	cgt Arg	act Thr	240
D		aag Lys 60															288
10	aac Asn 75	gtc Val	tgt Cys	tct Ser	Gly ggg	aaa Lys 80	aaa Lys	caa Gln	ccc Pro	agc Ser	agg Arg 85	aag Lys	gac Asp	aga Arg	aaa Lys	90 999	336
15		act Thr															384
20		cgt Arg	tag														393
25	<21 <21	0> 10 1> 13 2> PI 3> ro	30 RT	=													
23	\ <b>2</b> 1.	J / I \	Jacin	_													
30		0> 10 Gln		Ala	Gly	Leu	Thr	Leu -15	Met	Ala	Val	Ala	Val -10	Суѕ	Val	Ala	
30	Phe	Gln -5	Thr	Ser	Glu	Ala -1	Ile 1	Leu	Pro	Met	Ala 5	Ser	Ser	Cys	Cys	Thr 10	
35	Glu	Val	Ser	His	His 15	Val	Ser	Gly	Arg	Leu 20	Leu	Glu	Arg	Val	Ser 25	Ser	
	Cys	Ser	Ile	Gln 30	Arg	Ala	Asp	Gly	Asp 35	Суѕ	Asp	Leu	Ala	Ala 40	Val	Ile	
40	Leu	His	Val 45	Lys	Arg	Arg	Arg	Ile 50	Cys	Ile	Ser	Pro	His 55	Asn	Arg	Thr	
45	Leu	Lys 60	Gln	Trp	Met	Arg	Ala 65	Ser	Glu	Val	Lys	Lys 70	Asn	Gly	Arg	Glu	
	Asn 75	Val	Cys	Ser	Gly	Lys 80	Lys	Gln	Pro	Ser	Arg 85	Lys	Asp	Arg	Lys	Gly 90	
50	His	Thr	Thr	Arg	Lys 95	His	Arg	Thr	Arg	Gly 100	Thr	His	Arg	His	Glu 105	Ala	
	Ser	Arg															
55	<21	0 > 1 1 > 3 2 > D	62														

The control control control of the control con

	<213	3 > pı	cimat	e													
5		)> L> CI 2> (:		(336)	ı												
10		)> L> ma 2> (*															
10	atg		999			acc Thr											48
15	ctg Leu	agc Ser	cca Pro	gac Asp -5	cct Pro	aca Thr	gca Ala	gca Ala -1	ttc Phe 1	cta Leu	ctg Leu	cca Pro	ccc Pro 5	agc Ser	act Thr	gcc Ala	96
20						tac Tyr											144
25	aag Lys 25	gtc Val	atc Ile	cag Gln	gtg Val	gaa Glu 30	ctg Leu	cag Gln	gag Glu	gct Ala	gac Asp 35	ggg Gly	gac Asp	tgt Cys	cac His	ctc Leu 40	192
30						cac His											240
35	cag Gln	aac Asn	ccc Pro	agc Ser 60	ctg Leu	tca Ser	cag Gln	tgg Trp	ttt Phe 65	gag Glu	cac His	caa Gln	gag Glu	aga Arg 70	aag Lys	ctc Leu	288
	cat His	ggg Gly	act Thr 75	ctg Leu	ccc Pro	aag Lys	ctg Leu	aat Asn 80	ttt Phe	Gly ggg	atg Met	cta Leu	agg Arg 85	aaa Lys	atg Met	ggc Gly	336
40	tga	agcc	cca a	atago	ccaa	at aa	ataaa	a									362
45	<21 <21	0 > 12 1 > 13 2 > P1 3 > p3	12 RT	ce													
		0> 1: Lys		Pro	Pro -20	Thr	Phe	Cys	Ser	Leu -15	Leu	Leu	Leu	Ser	Leu -10	Leu	
50	Leu	Ser	Pro	Asp -5	Pro	Thr	Ala	Ala -1	Phe 1	Leu	Leu	Pro	Pro 5	Ser	Thr	Ala	
55	Cys	Cys 10	Thr	Gln	Leu	Tyr	Arg 15	Lys	Pro	Leu	Ser	Asp 20	Lys	Leu	Leu	Arg	
	Lys	Val	Ile	Gln	Val	Glu	Leu	Gln	Glu	Ala	Asp	Gly	Asp	Cys	His	Leu	

some and some size of the sound among the sound to the sound of the so

	Gln	Ala	Phe	Val	Leu 45	His	Leu	Ala	Gln	Arg 50	Ser	Ile	Cys	Ile	His 55	Pro	
5	Gln	Asn	Pro	Ser 60	Leu	Ser	Gln	Trp	Phe 65	Glu	His	Gln	Glu	Arg 70	Lys	Leu	
1.0	His	Gly	Thr 75	Leu	Pro	Lys	Leu	Asn 80	Phe	Gly	Met	Leu	Arg 85	Lys	Met	Gly	
10	<213 <212	0> 13 L> 43 2> Di 3> ro	33	5													
15		L> CI	OS 23).	. (382	2)												
20	<222	L> ma 2> (9	at_pe 98).	_													
25		)> 1: acct		ggctg	gagto	ga go		t Met					r Pro			c agc r Ser	52
30	ctc Leu -15	ccg Pro	ctg Leu	tta Leu	ctg Leu	ttg Leu -10	ctt Leu	ctg Leu	agc Ser	ccg Pro	gct Ala -5	cct Pro	gaa Glu	gca Ala	gcc Ala -1	ttg Leu 1	100
35	cct Pro	ctg Leu	ccc Pro	tcc Ser 5	agc Ser	act Thr	agc Ser	tgc Cys	tgt Cys 10	act Thr	cag Gln	ctc Leu	tat Tyr	aga Arg 15	cag Gln	cca Pro	148
40	ctc Leu	cca Pro	agc Ser 20	agg Arg	ctg Leu	ctg Leu	agg Arg	agg Arg 25	att Ile	gtc Val	cac His	atg Met	gaa Glu 30	ctg Leu	cag Gln	gag Glu	196
40	gcc Ala	gat Asp 35	gly ggg	gac Asp	tgt Cys	cac His	ctc Leu 40	cag Gln	gct Ala	gtc Val	gtg Val	ctt Leu 45	cac His	ctg Leu	gct Ala	cgg Arg	244
45	cgc Arg 50	agt Ser	gtc Val	tgt Cys	gtt Val	cat His 55	ccc Pro	cag Gln	aac Asn	cgc Arg	agc Ser 60	ctg Leu	gct Ala	cgg Arg	tgg Trp	tta Leu 65	292
50	gaa Glu	cgc Arg	caa Gln	ggg Gly	aaa Lys 70	agg Arg	ctc Leu	caa Gln	gly ggg	act Thr 75	gta Val	ccc Pro	agt Ser	tta Leu	aat Asn 80	ctg Leu	340
55	gta Val	cta Leu	caa Gln	aag Lys 85	aaa Lys	atg Met	tac Tyr	tca Ser	aac Asn 90	ccc Pro	caa Gln	cag Gln	caa Gln	aac Asn 95			382
	taai	taaa	gca i	acati	taga	cg a	caaaa	aaaa	a aa	aaaa	aaaa	aaaa	aaaa	aaa a	a		433

5	<2 <2 <2 <2
10	<4 Me -2 Le
15	Se Ar
20	Le 4
25	Pr Le
30	Ту
	<2

the control of the co

14

5	<210: <211: <212: <213:	> 12 > PR	0 T	:												
10	<4000 Met N -25			Gly	Leu	Ser -20	Pro	Ala	Ser	Ser	Leu -15	Pro	Leu	Leu	Leu	Leu -10
10	Leu I	Leu	Ser	Pro	Ala -5	Pro	Glu	Ala	Ala -1	Leu 1	Pro	Leu	Pro	Ser 5	Ser	Thr
15	Ser (	Cys	Cys 10	Thr	Gln	Leu	Tyr	Arg 15	Gln	Pro	Leu	Pro	Ser 20	Arg	Leu	Leu
	Arg A	Arg 25	Ile	Val	His	Met	Glu 30	Leu	Gln	Glu	Ala	Asp 35	Gly	Asp	Cys	His
20	Leu (	Gln	Ala	Val	Val	Leu 45	His	Leu	Ala	Arg	Arg 50	Ser	Val	Cys	Val	His 55
25	Pro (	Gln	Asn	Arg	Ser 60	Leu	Ala	Arg	Trp	Leu 65	Glu	Arg	Gln	Gly	Lys 70	Arg
23	Leu (	Gln	Gly	Thr 75	Val	Pro	Ser	Leu	Asn 80	Leu	Val	Leu	Gln	Lys 85	Lys	Met
30	Tyr S	Ser	Asn 90	Pro	Gln	Gln	Gln	Asn 95								
35	<211: <212:	<210> 15 <211> 32 <212> DNA <213> primate														
40		<400> 15: ATCTGGCACC ACACCTTCTA CAATGAGCTG CG														
45	<210: <211: <212: <213:	> 32 > DN	! IA	:e												

32

50

<400> 16 CGTCATACTC CTGCTTGCTG ATCCACATCT GC